

## AMENDMENTS TO THE CLAIMS

### 1. (Canceled)

**2. (Currently amended):** A method for estimating the precision of measurements taken from a gene expression microarray ~~an array~~, comprising:

- (a) identifying a set of low-level data measurements;
- (b) estimating a standard deviation,  $\sigma_\epsilon$  of an additive error component,  $\epsilon$  ;
- (c) estimating a background parameter,  $\alpha$  ;
- (d) identifying a set of replicated high-level data measurements;
- (e) estimating a standard deviation,  $\sigma_\eta$  , of a proportional error component,  $\eta$

from the standard deviation of the logarithm of the replicated high-level data set;

(f) measuring a signal,  $y$ , wherein said signal indicates an amount of a biological molecule; and

- (g) estimating a variance of the measured signal as

$$Var\{y\} = \mu^2 e^{\sigma_\eta^2} (e^{\sigma_\eta^2} - 1) + \sigma_\epsilon^2$$

wherein  $\mu$  is the amount of the biological molecule and

$$y = \alpha + \mu e^\eta + \epsilon$$

and wherein said identifying step (a) comprises the use of a thresholding algorithm to establish a cutoff, and the set of low-level data consists of those data with values less than the cutoff.

**3. (Currently amended):** The method of claim 2, wherein the thresholding algorithm comprises the steps of:

(a) identifying  $A_N$ , an initial set of low-level data measurements consisting of  $q$  percent of the total number of data points having the lowest measurement values,  $A_N = \{x_1, x_2, \dots, x_{no}\}$ ;

- (b) calculating a mean and a standard deviation of the initial set;

(c) calculating a cutoff point,  $u_N = \text{mean} + (c \times \text{the standard deviation})$ ,  
 wherein  $c$  is the number of standard deviations or mean absolute deviations above the  
mean or median and  $c$  is set at 2, 2.5 or 3 for each iteration of the thresholding algorithm  
 $2 \leq c \leq 3$ ;

(d) defining a new set,  $A_{N+1} = \{x_j < u_N\}$ ;

(e) calculating a mean and standard deviation of the new set; and

(f) repeating steps (c) and (d) using the mean and standard deviation of the  
 new set until the algorithm converges.

**4. (Currently amended):** The method of claim 2, wherein the thresholding  
 algorithm comprises the steps of:

(a) identifying  $A_N$ , an initial set, of low-level data consisting of  $q$  percent of  
 the total number of data points having the lowest measurement values,  $A_N = \{x_1, x_2, \dots,$   
 $x_{no}\}$ ;

(b) calculating a median of the initial set,  $m_o = \text{median } \{x_j\}_{j=1}^{n_o}$  and a median of  
 the absolute deviations about the median,  $MAD_o = \text{median } \{|x_j - m_o|\}_{j=1}^{n_o}$ ;

(c) calculating a cutoff point,  $u_o = MAD_o + (c \times s_o)$ , wherein  $s_o = MAD_o/0.675$   
 and  $c$  is the number of standard deviations or mean absolute deviations above the mean or  
median and  $c$  is set at 2, 2.5 or 3 for each iteration of the thresholding algorithm  $2 \leq c \leq 3$ ;

(d) defining a new set,  $A_{N+1} = \{x_j < u_N\}$ ;

(e) calculating a median and a median of the absolute deviations about the  
 median of the new set; and

(f) repeating steps (c) and (d) using the median and the median of the absolute  
 deviations about the median of the new set until the algorithm converges.

**5. (Original):** The method of claim 2, wherein the mean of the low-level data  
 measurements is used as the estimate of the background parameter,  $\alpha$ .

**6. (Previously presented):** The method of claim 2, wherein the standard deviation of the low-level data measurements is used as the estimate of the parameter  $\sigma_e$ .

**7. (Previously presented):** The method of claim 2, wherein a mean of negative control data is used as the estimate of the background parameter,  $\alpha$ .

**8. (Previously presented):** The method of claim 2, wherein the biological molecule is a nucleic acid.

**9. (Original):** The method of claim 8, wherein the nucleic acid is mRNA.

**10. (Original):** The method of claim 8, wherein the biological molecule is DNA.

**11. (Original):** The method of claim 10, wherein the DNA is cDNA.

**12. (Original):** The method of claim 10, wherein the DNA is genomic.

**13. (Canceled)**

**14. (Canceled)**